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☐ 1: CAA54576. N2042 [Saccharomy...[gi:496725]

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LOCUS CAA54576 661 aa .linear PLN 24-MAY-1995
 DEFINITION N2042 [Saccharomyces cerevisiae].
 ACCESSION CAA54576
 VERSION CAA54576.1 GI:496725
 DBSOURCE embi locus SCN201952, accession X77395.1
 KEYWORDS

SOURCE Saccharomyces cerevisiae (baker's yeast)
 ORGANISM Saccharomyces cerevisiae
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Saccharomyces.

REFERENCE 1
 AUTHORS Verhasselt, P., Aert, R., Voet, M. and Volckaert, G.
 TITLE Twelve open reading frames revealed in the 23.6 kb segment flanking
 the centromere on the Saccharomyces cerevisiae chromosome XIV right
 arm

JOURNAL Yeast 10 (10), 1355-1361 (1994)

MEDLINE 95208356

PUBMED 7900425

REFERENCE 2 (residues 1 to 661)

AUTHORS Volckaert, G.

TITLE Direct Submission

JOURNAL Submitted (31-JAN-1994) G. Volckaert, Laboratory of Gene
 Technology, Catholic University of Leuven, W. Decrolyaan 42, 3001
 Leuven, BELGIUM

FEATURES Location/Qualifiers
 .source 1..661
 /organism="Saccharomyces cerevisiae"
 /strain="FY1679"
 /db_xref="taxon:4932"
 /chromosome="XIV"
 /map="centromeric region (right arm)"
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 CDS 1..661
 /gene="N2042"
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 /db_xref="SGD:S0005291"
 /db_xref="SWISS-PROT:P40345"

ORIGIN

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121 ylddwkdvlp  qgissfiddi  qagnystssl  ddlsenfavg  kqlrldynie  akhpvvmvpg
181 vistgieswg  vigddecdss  ahfrkrlwgs  fymrltmvmd  kvcwlkhvml  dpetgldppn
241 ftlraaqqfe  stdyfiagyw  iwnkvfqnlq  vigyepnkmt  saaydwrlay  ldlerdryf
301 tkлкеqielf  hqlsgkvcl  ighsmgsqii  fyfmkwveae  gplyngggrg  wvnehidsfi
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421 geeviwgdmk  sssedalnnn  tdygnfirf  erntsdafnk  nltmkdainm  tllsispewlq
481 rrvheqysfg  yskneeelrk  nelhhkhwsn  pmevplpeap  hmkiyciygv  nnptarayvy
541 keeddssaln  ltidyekqp  vfltegdgtv  plvahsmchk  waqgaspynp  aginvtivem
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661 m

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//

Sep 16 2003 13:15:10

DNA is known in yeast

LOCUS SCN201952 23901 bp DNA linear PLN 24-MAY-1995
 DEFINITION S.cerevisiae N2019, N2021, N2023, N2025, N2027, N2031, N2048 and N2050 genes.
 ACCESSION X77395
 VERSION X77395.1 GI:496717
 KEYWORDS mitochondrial citrate synthase; PRP2 gene; RNA polymerase III; RNA-dependent ATPase; rpc34 gene; tau34 protein; tRNA-Asn; tRNA-Pro; uridine kinase; URK1 gene; yun34 gene.
 SOURCE Saccharomyces cerevisiae.
 ORGANISM Saccharomyces cerevisiae
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 REFERENCE 1 (bases 1 to 23901)
 AUTHORS Verhasselt, P., Aert, R., Voet, M. and Volckaert, G.
 TITLE Twelve open reading frames revealed in the 23.6 kb segment flanking the centromere on the Saccharomyces cerevisiae chromosome XIV right arm
 JOURNAL Yeast 10 (10), 1355-1361 (1994)
 REFERENCE 2 (bases 1 to 23901)
 AUTHORS Volckaert, G.
 TITLE Direct Submission
 JOURNAL Submitted (31-JAN-1994) G. Volckaert, Laboratory of Gene Technology, Catholic University of Leuven, W. Decrolyaan 42, 3001 Leuven, BELGIUM

Query Match 100.0%; Score 1986; DB 8; Length 23901;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1986; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGGCACACTGTTTCGAAGAAATGTCCAGAACCAAAGAGTGATTCTGATGAAAACAAT 60
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 Db 11755 ATGGGCACACTGTTTCGAAGAAATGTCCAGAACCAAAGAGTGATTCTGATGAAAACAAT 11814
 Qy 61 AAAGGGGGTTCTGTTTCATAACAAGCGAGAGAGCAGAAACCACATTCATCATCAACAGGGA 120
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 Db 11815 AAAGGGGGTTCTGTTTCATAACAAGCGAGAGAGCAGAAACCACATTCATCATCAACAGGGA 11874
 Qy 121 TTAGGCCATAAGAGAAGAAGGGGTATTAGTGGCAGTGCAAAAAGAAATGAGCGTGGCAAA 180
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 Qy 301 GTTCATAATAGCGATAGCGACTTGTTTGACAACCTTTGTAAATTTTGATTCACTTAAAGTG 360
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 Db 12055 GTTCATAATAGCGATAGCGACTTGTTTGACAACCTTTGTAAATTTTGATTCACTTAAAGTG 12114
 Qy 361 TATTTGGATGATTGGAAAGATGTTCTCCACAAGGTATAAGTTCGTTTATTGATGATATT 420
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Db	12235	AAACAACCTCTTACGTGATTATAATATCGAGGCCAAACATCCTGTTGTAATGGTTCCTGGT	12294
Qy	541	GTCATTTCTACGGGAATTGAAAGCTGGGGAGTTATTGGAGACGATGAGTGCGATAGTTCT	600
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Qy	601	GCGCATTTTCGTAAACGGCTGTGGGGAAGTTTTTACATGCTGAGAACAATGGTTATGGAT	660
Db	12355	GCGCATTTTCGTAAACGGCTGTGGGGAAGTTTTTACATGCTGAGAACAATGGTTATGGAT	12414
Qy	661	AAAGTTTGTTGGTTGAAACATGTAATGTTAGATCCTGAAACAGGTCTGGACCCACCGAAC	720
Db	12415	AAAGTTTGTTGGTTGAAACATGTAATGTTAGATCCTGAAACAGGTCTGGACCCACCGAAC	12474
Qy	721	TTTACGCTACGTGCAGCACAGGGCTTCGAATCAACTGATTATTTTCATCGCAGGGTATTGG	780
Db	12475	TTTACGCTACGTGCAGCACAGGGCTTCGAATCAACTGATTATTTTCATCGCAGGGTATTGG	12534
Qy	781	ATTTGGAACAAAGTTTTCCAAAATCTGGGAGTAATTGGCTATGAACCCAATAAAATGACG	840
Db	12535	ATTTGGAACAAAGTTTTCCAAAATCTGGGAGTAATTGGCTATGAACCCAATAAAATGACG	12594
Qy	841	AGTGCTGCGTATGATTGGAGGCTTGCATATTTAGATCTAGAAAGACGCGATAGGTACTTT	900
Db	12595	AGTGCTGCGTATGATTGGAGGCTTGCATATTTAGATCTAGAAAGACGCGATAGGTACTTT	12654
Qy	901	ACGAAGCTAAAGGAACAAATCGAACTGTTTCATCAATTGAGTGGTGAAAAAGTTTGTTTA	960
Db	12655	ACGAAGCTAAAGGAACAAATCGAACTGTTTCATCAATTGAGTGGTGAAAAAGTTTGTTTA	12714
Qy	961	ATTGGACATTCTATGGGTTCTCAGATTATCTTTTACTTTATGAAATGGGTCGAGGCTGAA	1020
Db	12715	ATTGGACATTCTATGGGTTCTCAGATTATCTTTTACTTTATGAAATGGGTCGAGGCTGAA	12774
Qy	1021	GGCCCTCTTTACGGTAATGGTGGTTCGTGGCTGGGTTAACGAACACATAGATTCATTTCATT	1080
Db	12775	GGCCCTCTTTACGGTAATGGTGGTTCGTGGCTGGGTTAACGAACACATAGATTCATTTCATT	12834
Qy	1081	AATGCAGCAGGGACGCTTCTGGGCGCTCCAAAGGCAGTTCCAGCTCTAATTAGTGGTGAA	1140
Db	12835	AATGCAGCAGGGACGCTTCTGGGCGCTCCAAAGGCAGTTCCAGCTCTAATTAGTGGTGAA	12894
Qy	1141	ATGAAAGATACCATTCGAATTAAATACGTTAGCCATGTATGGTTTGAAAAGTTCTTCTCA	1200
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Qy	1201	AGAATTGAGAGAGTAAAAATGTTACAAACGTGGGGTGGTATACCATCAATGCTACCAAAG	1260
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Qy	1261	GGAGAAGAGGTCATTTGGGGGGATATGAAGTCATCTTCAGAGGATGCATTGAATAACAAC	1320
Db	13015	GGAGAAGAGGTCATTTGGGGGGATATGAAGTCATCTTCAGAGGATGCATTGAATAACAAC	13074
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Db	13075	ACTGACACATACGGCAATTTTCATTCGATTTGAAAGGAATACGAGCGATGCTTTCAACAAA	13134
Qy	1381	AATTTGACAATGAAAGACGCCATTAACATGACATTATCGATATCACCTGAATGGCTCCAA	1440
Db	13135	AATTTGACAATGAAAGACGCCATTAACATGACATTATCGATATCACCTGAATGGCTCCAA	13194
Qy	1441	AGAAGAGTACATGAGCAGTACTCGTTCGGCTATTCCAAGAATGAAGAAGAGTTAAGAAAA	1500
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Qy	1501	AATGAGCTACACCACAAGCACTGGTCGAATCCAATGGAAGTACCACTTCCAGAAGCTCCC	1560
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Db	13315	CACATGAAAATCTATTGTATATACGGGGTGAACAACCCAACTGAAAGGGCATATGTATAT	13374
Qy	1621	AAGGAAGAGGATGACTCCTCTGCTCTGAATTTGACCATCGACTACGAAAGCAAGCAACCT	1680
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Db	13435	GTATTCCTCACCGAGGGGGACGGAACCGTTCGGCTCGTGGCGCATTC AATGTGTACAAA	13494
Qy	1741	TGGGCCCAGGGTGCTTCACCGTACAACCCTGCCGGAATTAACGTTACTATTGTGGAAATG	1800
Db	13495	TGGGCCCAGGGTGCTTCACCGTACAACCCTGCCGGAATTAACGTTACTATTGTGGAAATG	13554
Qy	1801	AAACACCAGCCAGATCGATTTGATATACGTGGTGGAGCAAAAAGCGCCGAACACGTAGAC	1860
Db	13555	AAACACCAGCCAGATCGATTTGATATACGTGGTGGAGCAAAAAGCGCCGAACACGTAGAC	13614
Qy	1861	ATCCTCGGCAGCGCGGAGTTGAACGATTACATCTTGAAAATTGCAAGCGGTAATGGCGAT	1920
Db	13615	ATCCTCGGCAGCGCGGAGTTGAACGATTACATCTTGAAAATTGCAAGCGGTAATGGCGAT	13674
Qy	1921	CTCGTCGAGCCACGCCAATTGTCTAATTTGAGCCAGTGGGTTTCTCAGATGCCCTTCCCA	1980
Db	13675	CTCGTCGAGCCACGCCAATTGTCTAATTTGAGCCAGTGGGTTTCTCAGATGCCCTTCCCA	13734
Qy	1981	ATGTAA	1986
Db	13735	ATGTAA	13740